

Appendix V

Alignment of instant SEQ ID NO: 1 (nucleotides 1-780) with SEQ ID NO: 1 of Sisk et al. Note: Sisk et al teach a circular plasmid of SEQ ID NO: 1, and the total length of SEQ ID NO: 1 is 6069 nucleotides. Accordingly, nucleotide 6069 is contiguous with nucleotide 1 of Sisk et al.

Score = 1336 bits (723), Expect = 0.0
Identities = 723/723 (100%), Gaps = 0/723 (0%)
Strand=Plus/Plus

Query	58	AGCTTGATGATTGATTATGACTAGTATATTAATAGTATATCAATTAACGGGGTCATTAGTGCA	117
Sbjct	1	AGCTTGACATTGCTTATTGACTAGTATATTAATAGTATATCAATTAACGGGGTCATTAGTGCA	60
Query	118	TAGGCCCATATATGGAGTTCGGCGTTACATAACAATTACGGTAAATGGCCGCGCTGCTGACC	177
Sbjct	61	TAGCCCATATATGGAGTTCGGCGTTACATAACAATTACGGTAAATGGCCGCGCTGCTGACC	120
Query	178	GCCCAACGACCCCGCCGATTCAGTCTAATAATGACGATGCTCCCATATGACCGCAAT	237
Sbjct	121	GCCCAACGACCCCGCCGATTCAGTCTAATAATGACGATGCTCCCATATGACCGCAAT	180
Query	239	AGGGAATTTTCATTGACGTCAATGGGTGGAGTATTACGGTAACTGCCCACTTGGCAST	297
Sbjct	181	AGGGAATTTTCATTGACGTCAATGGGTGGAGTATTACGGTAACTGCCCACTTGGCAST	240
Query	299	ACATCAAGTGTATCATATGCCAAGTAGCGCCCCCTATTGACGTCAATGACGGTAAATGGCC	357
Sbjct	241	ACATCAAGTGTATCATATGCCAAGTAGCGCCCCCTATTGACGTCAATGACGGTAAATGGCC	300
Query	358	CGCTGGCAATTATGGCCAGTACATGACCTTATGGGAATTTCTACTTGGCAGTACATCTA	417
Sbjct	301	CGCTGGCAATTATGGCCAGTACATGACCTTATGGGAATTTCTACTTGGCAGTACATCTA	360
Query	418	CGTATTAGTACTGCTATTACCATGGTGATGCGGTTTTCGCASTACATCAATGGCGCTGG	477
Sbjct	361	CGTATTAGTACTGCTATTACCATGGTGATGCGGTTTTCGCASTACATCAATGGCGCTGG	420
Query	478	ATACGGGTTTGACTACGCGGAGATTCTCAAGTCTCCACCCCTTGGAGTCAATGGGAATTT	537
Sbjct	421	ATACGGGTTTGACTACGCGGAGATTCTCAAGTCTCCACCCCTTGGAGTCAATGGGAATTT	480
Query	538	GTTTTCGACCAAAATCAACGGGACTTTCCAAATGTCGTAAACAATCCGCCCAATTGAC	597
Sbjct	481	GTTTTCGACCAAAATCAACGGGACTTTCCAAATGTCGTAAACAATCCGCCCAATTGAC	540
Query	598	GCAAAATGGCGGTATGGCTGTACGTTGGGAGTCTATATAAGACAGAGCTGTTTAGTGA	657
Sbjct	541	GCAAAATGGCGGTATGGCTGTACGTTGGGAGTCTATATAAGACAGAGCTGTTTAGTGA	600
Query	658	CGCTCAGATCGCTGGAGACGCCATTCACGCTGTTTTCGACCTCATAGAAGACACCGGA	717
Sbjct	601	CGCTCAGATCGCTGGAGACGCCATTCACGCTGTTTTCGACCTCATAGAAGACACCGGA	660
Query	718	CGGATCCAGCTCCGCGGCGCGGGAACGGTGCAATTGGAACGCGGATTCGCCGTGCCAAG	777
Sbjct	661	CGGATCCAGCTCCGCGGCGCGGGAACGGTGCAATTGGAACGCGGATTCGCCGTGCCAAG	720
Query	778	TGA	780
Sbjct	721	TGA	723

Score = 99.0 bits (53), Expect = 7e-24
Identities = 53/53 (100%), Gaps = 0/53 (0%)
Strand=Plus/Plus

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Query 5      TGTGAGCGGATAACAATTTTCACACAGGAACAGCTATGACCATGATTACGCCA 57
              |||
Sbjct 6017   TGTGAGCGGATAACAATTTTCACACAGGAACAGCTATGACCATGATTACGCCA 6069

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